



## SEQUENCE LISTING

<10> LEUNG, Shui-on  
HANSEN, Hans

<120> IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL  
LYMPHOMA AND LEUKEMIA CELLS

<130> 40923-0048US3

<140> US 09/741,843

<141> 2000-12-22

<150> US 09/127,902

<151> 1998-08-03

<150> US 08/690,102

<151> 1996-07-31

<150> US 08/289,576

<151> 1994-08-12

<160> 25

<170> PatentIn version 3.1

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<213> Murinae gen. sp.

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gaa aac gtc act atg agc tgt aag tcc agt caa agt gtt tta tac agt 96  
Glu Asn Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser  
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gca aat cac aag aac tac ttg gcc tgg tac cag cag aaa cca ggg cag 144  
Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
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tct cct aaa ctg ctg atc tac tgg gca tcc act agg gaa tct ggt gtc 192  
Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
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cct gat cgc ttc aca ggc agc gga tct ggg aca gat ttt act ctt acc 240  
Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

atc agc aga gta caa gtt gaa gac ctg gca att tat tat tgt cac caa 288  
Ile Ser Arg Val Gln Val Glu Asp Leu Ala Ile Tyr Tyr Cys His Gln  
85 90 95

tac ctc tcc tcg tgg acg ttc ggt gga ggg acc aag ctg gag atc aaa 336  
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Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
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Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
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Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
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Ile Ser Arg Val Gln Val Glu Asp Leu Ala Ile Tyr Tyr Cys His Gln  
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tca gtg aag atg tcc tgc aag gct tct ggc tac acc ttt act agc tac      96
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
          20          25          30

tgg ctg cac tgg ata aaa cag agg cct gga cag ggt ctg gaa tgg att     144
Trp Leu His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
          35          40          45

gga tac att aat cct agg aat gat tat act gag tac aat cag aac ttc     192
Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
          50          55          60

aag gac aag gcc aca ttg act gca gac aaa tcc tcc agc aca gcc tac     240
Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
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atg caa ctg agc agc ctg aca tct gag gac tct gca gtc tat tac tgt     288
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
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gca aga agg gat att act acg ttc tac tgg ggc caa ggc acc act ctc     336
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          35          40          45

Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
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Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr  
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Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys  
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Thr Val Ser Ser  
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gca cct aaa ctg ctg atc tac ttg gca tcc act agg gaa tct ggt gtc 192  
Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60  
cct tcg cga ttc tct ggc agc gga tct ggg aca gat ttt act ttc acc 240  
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr  
65 70 75 80  
atc agc tct ctt caa cca gaa gac att gca aca tat tat tgt cac caa 288  
Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln  
85 90 95  
tac ctc tcc tcg tgg acg ttc ggt gga ggg acc aag gtg cag atc aaa 336  
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100 105 110  
cgt 339  
Arg

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 35 40 45

Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
 50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr  
 65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln  
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Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Val Gln Ile Lys  
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Arg

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tca gtg aag gtc tcc tgc aag gct tct ggc tac acc ttt act agc tac 96  
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
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tgg ctg cac tgg gtc agg cag gca cct gga cag ggt ctg gaa tgg att 144  
 Trp Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile  
 35 40 45

gga tac att aat cct agg aat gat tat act gag tac aat cag aac ttc 192  
 Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe  
 50 55 60

aag gac aag gcc aca ata act gca gac gaa tcc acc aat aca gcc tac 240  
 Lys Asp Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr  
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atg gag ctg agc agc ctg agg tct gag gac acg gca ttt tat ttt tgt 288  
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys  
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gca aga agg gat att act acg ttc tac tgg ggc caa ggc acc acg gtc 336  
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 35 40 45

Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe  
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Lys Asp Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr  
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Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys  
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 35 40 45

Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe  
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Lys Asp Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr  
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys  
 85 90 95

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 agatccgctg cctgtgaagc gatcagggac accagattcc ctagtggatg cccagtagat 180  
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 cacagccaga gatgatggag actgggtcag ctgaatgctc 339  
  
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